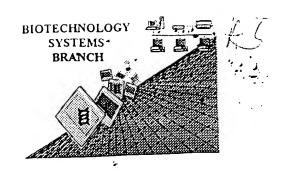# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____09/674,195___ **BEST AVAILABLE COPY**

Source: _____PCT_____

Date Processed by STIC: _____09/18/2001_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: O9/674 195A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWA

1____ Wrapped Nucleics Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length — Sequence(s)____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING   DATE: 09/18/2001
PATENT APPLICATION: US/09/674,195A   TIME: 13:30:00

Input Set : A:\14014.0325U2.TXT
Output Set: N:\CRF3\09182001\I674195A.raw

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 4 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS
 5        REPRESENTED BY THE
 6        SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
 7        CENTERS FOR
 8        DISEASE CONTROL AND PREVENTION
 9        Rosely M. Zancope-Oliveira
10        Timothy J. Lott
11        Leonard W. Mayer
12        Errol Reiss
13        George S. Deepe
17 <120> TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
18        HISTOPLASMA CAPSULATUM, ANTIGENS, VACCINES, AND ANTIBODIES,
19        METHODS AND KITS FOR DETECTING HISTOPLASMOSIS
22 <130> FILE REFERENCE: 14114.0325U2
24 <140> CURRENT APPLICATION NUMBER: 09/674,195A
25 <141> CURRENT FILING DATE: 2000-10-26
27 <150> PRIOR APPLICATION NUMBER: 60/083,676
28 <151> PRIOR FILING DATE: 1998-04-30
30 <150> PRIOR APPLICATION NUMBER: PCT/US99/09151
31 <151> PRIOR FILING DATE: 1999-04-27
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44 <222> LOCATION: (1)...(3862)
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 69 aaattcccca ggctgcaact gcacatgata cggcatggga tttcctcagc cagcagccca   1320
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 93 ccggggccgcg tttaacagcg ccaacaacaa agtagatatc gtcctagtgg gctcatcgct  2760
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124 Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
125         35                  40                  45
126 Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
127     50                  55                  60
128 Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
129 65                  70                  75                  80
130 Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
131             85                  90                  95
132 Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
133             100                 105                 110
134 Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
135         115                 120                 125
136 Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
137     130                 135                 140
138 Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
139 145                 150                 155                 160
140 Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
141             165                 170                 175
142 Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
143             180                 185                 190
144 Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
145         195                 200                 205
146 Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
147     210                 215                 220
148 Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
149 225                 230                 235                 240
150 Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
151             245                 250                 255
152 Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
153             260                 265                 270
154 His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
155         275                 280                 285
156 Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
157     290                 295                 300
158 Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
159 305                 310                 315                 320
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167     370                 375                 380
168 Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
169 385                 390                 395                 400
170 Asp Gly Ala Gly Gln Met Phe Ile Pro Leu Asn Thr Ala Ala Tyr Thr
171                 405                 410                 415
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173             420                 425                 430
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175         435                 440                 445
176 Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
177     450                 455                 460
178 Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
179 465                 470                 475                 480
180 Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
181             485                 490                 495
182 Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
183         500                 505                 510
184 Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
185         515                 520                 525
186 Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
187     530                 535                 540
188 Leu Arg Leu Asp Gly Leu Lys Ile Ala Leu Leu Thr Arg Asp Asp Gly
189 545                 550                 555                 560
190 Ser Phe Thr Ile Ala Glu Gln Leu Arg Ala Ala Phe Asn Ser Ala Asn
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192 Asn Lys Val Asp Ile Val Leu Val Gly Ser Ser Leu Asp Pro Gln Arg
193             580                 585                 590
194 Gly Val Asn Met Thr Tyr Ser Gly Ala Asp Gly Ser Ile Phe Asp Ala
195         595                 600                 605
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197     610                 615                 620
198 Arg Gly Arg Pro Leu Arg Ile Ile Thr Asp Ala Tyr Ala Tyr Gly Lys
199 625                 630                 635                 640
200 Pro Val Gly Ala Val Gly Asp Gly Ser Asn Glu Ala Leu Arg Asp Val
201             645                 650                 655
202 Leu Met Ala Ala Gly Gly Asp Ala Ser Asn Gly Leu Asp Gln Pro Gly
203             660                 665                 670
204 Val Tyr Ile Ser Asn Asp Val Ser Glu Ala Tyr Val Arg Ser Val Leu
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212 <211> LENGTH: 8
213 <212> TYPE: PRT
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272  1               5                   10
274 <210> SEQ ID NO: 10
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*A 213 response of Unknown Requires an
~~223~~ explanation or description in field
223.*

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/674,195A**

DATE: 09/18/2001
TIME: 13:30:02

Input Set : **A:\14014.0325U2.TXT**
Output Set: **N:\CRF3\09182001\I674195A.raw**

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